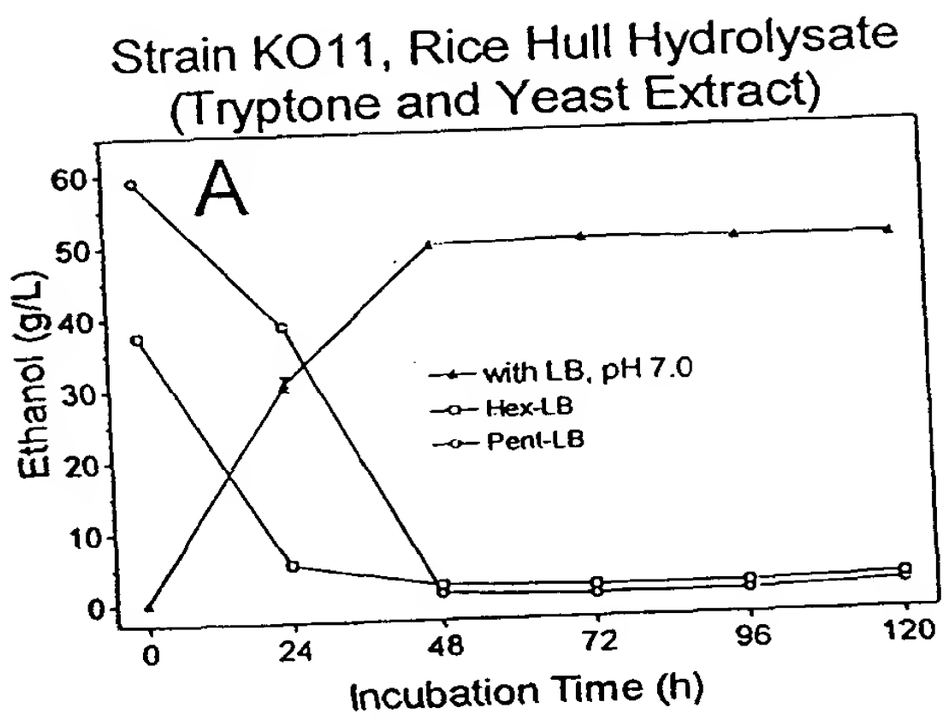
Fig. 1


Strain KO11, Rice Hull Hydrolysate
(Tryptone and Yeast Extract)
A
Ethanol (g/L)
Incubation Time (h)
with LB, pH 7.0
Hex-LB
Pent-LB
0
10
20
30
40
50
60
0
24
48
72
96
120

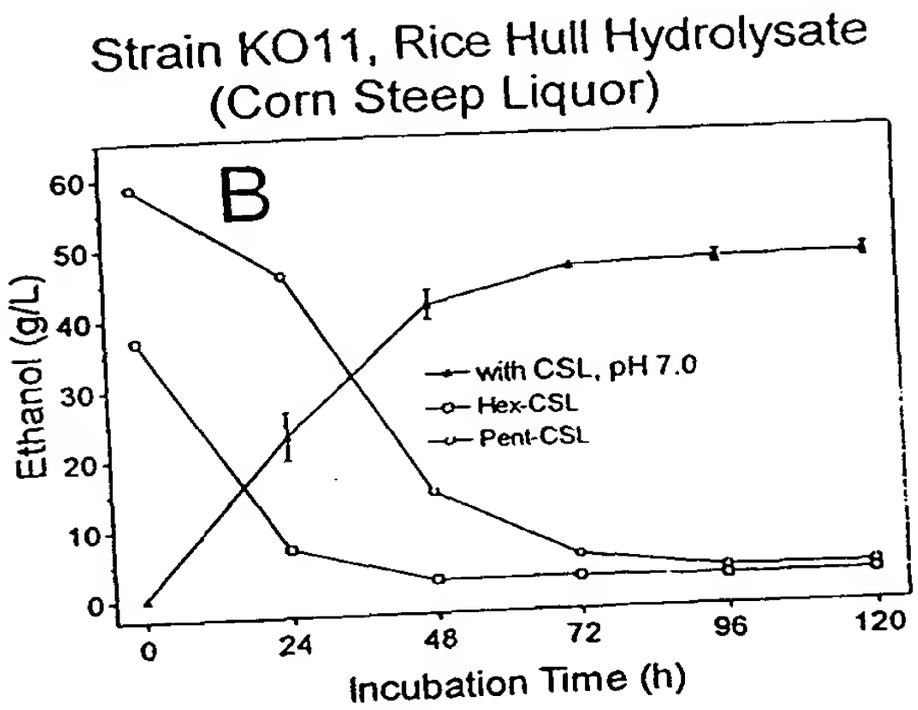

Strain KO11, Rice Hull Hydrolysate
(Corn Steep Liquor)
B
Ethanol (g/L)
Incubation Time (h)
with CSL, pH 7.0
Hex-CSL
Pent-CSL
0
10
20
30
40
50
60
0
24
48
72
96
120

Fig. 2

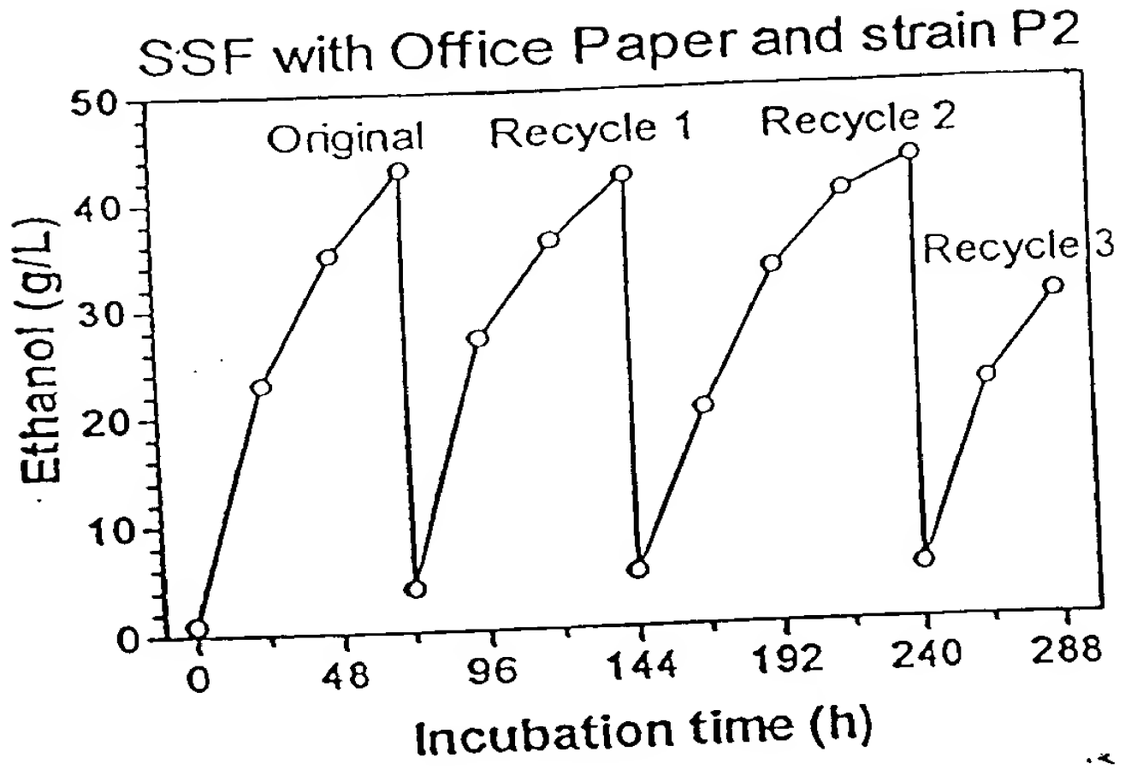

SSF with Office Paper and strain P2
Ethanol (g/L)
50
40
30
20
10
0
Original
Recycle 1
Recycle 2
Recycle 3
0
48
96
144
192
240
288
Incubation time (h)

Fig. 3

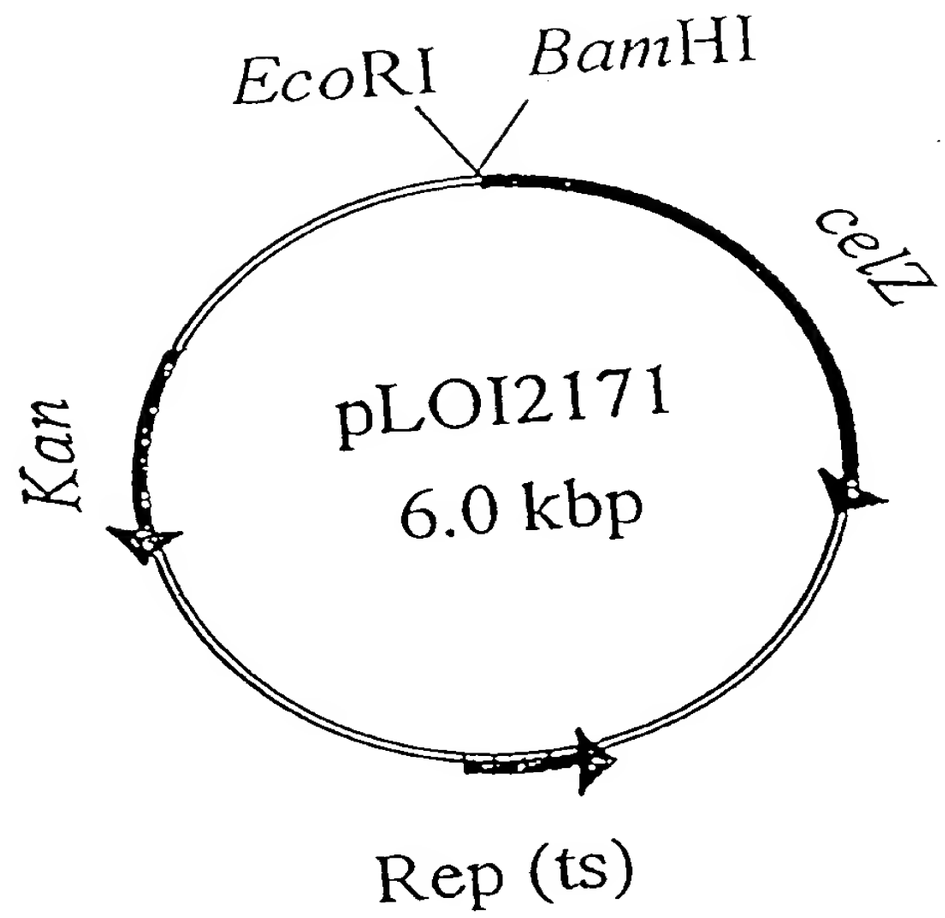


Fig. 4

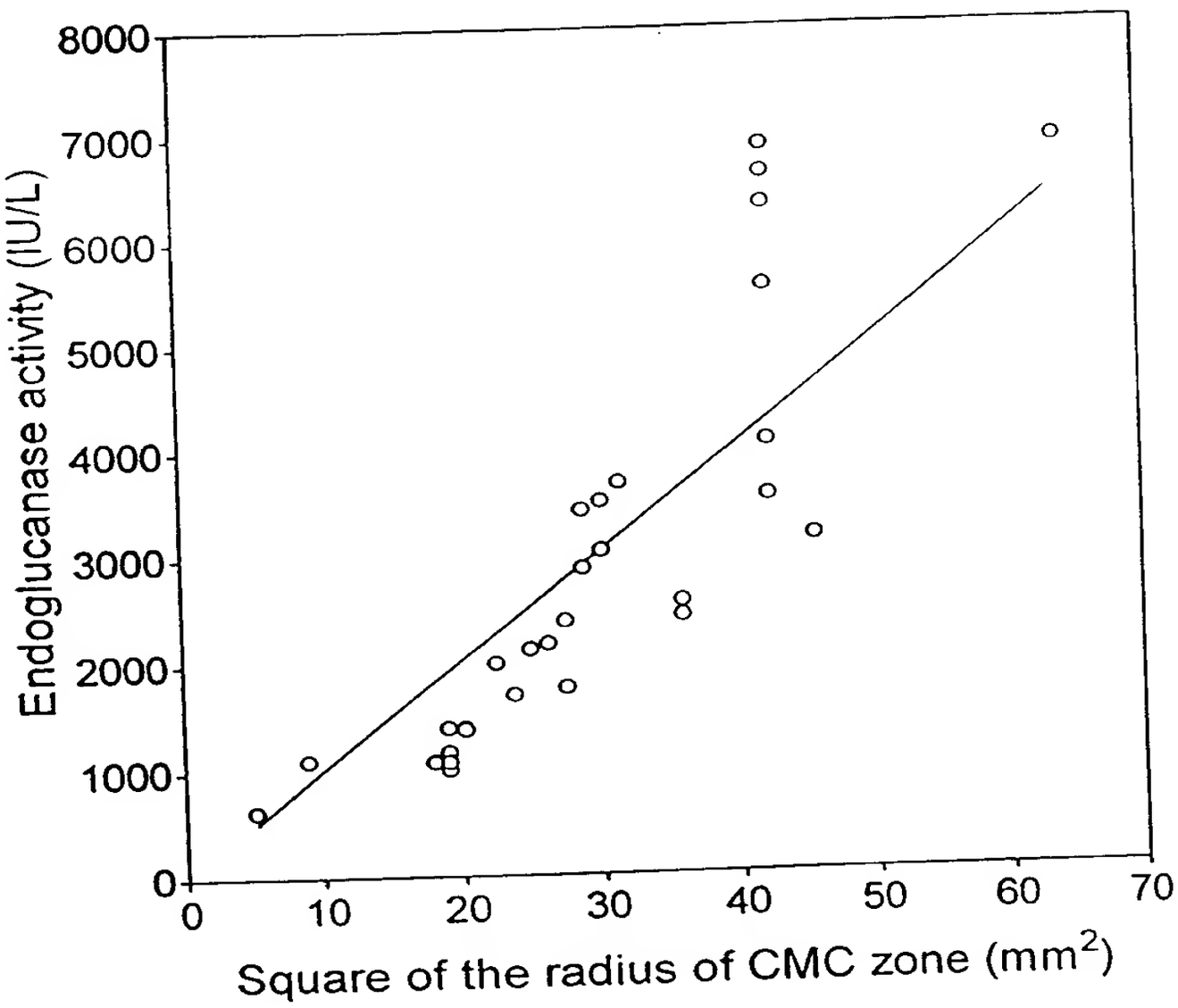

8000
7000
6000
5000
4000
3000
2000
1000
0
Endoglucanase activity (IU/L)
0
10
20
30
40
50
60
70
Square of the radius of CMC zone (mm2)

Fig. 5

-35 region -10 region #

1051 CTTTTTCGGC ATGAGCAACC AACATTTTCA AGGTATCATC CTGATGCGCA

1101 ATATCGGCAT CGGTTAGCCA TAACCATTTT ACCTGTCCGG CGGCCTTAAT
1151 ACCTTGATCA GATGGTTCGT GGTGTTGTTA CCTTGCCGAA GGGCACCGGT
1201 AAAAATGTTC GCGTCGGTGT TTTCGCCCGT GGCCCGAAAG CTGAAGAAGC
1251 TAAAGCTGCT GGTGCAGAAG TTGTCGGCGC AGAAGACCTG ATGGAAGCCA

-35 region -10 region

1301 TTCAGGGCGG CAGCATTGAT TTCGATCGTG ATGCCCTTTA TACTGAAATT

#

1351 GCCTTGCGCT GCCATAATGA AGCAGCCTCC GGTGTTTTGG CAGATTTAAG

Shine-Dalgarno

1401 CGCTGCCTGA TTTTCGTgat cctctagagt ctatgaaatg gagattcatt

celZ coding region–>

1451 t*atgcctctc tcttattcgg ataaccatcc agtcatccgc aagcttggcc*

Fig. 6

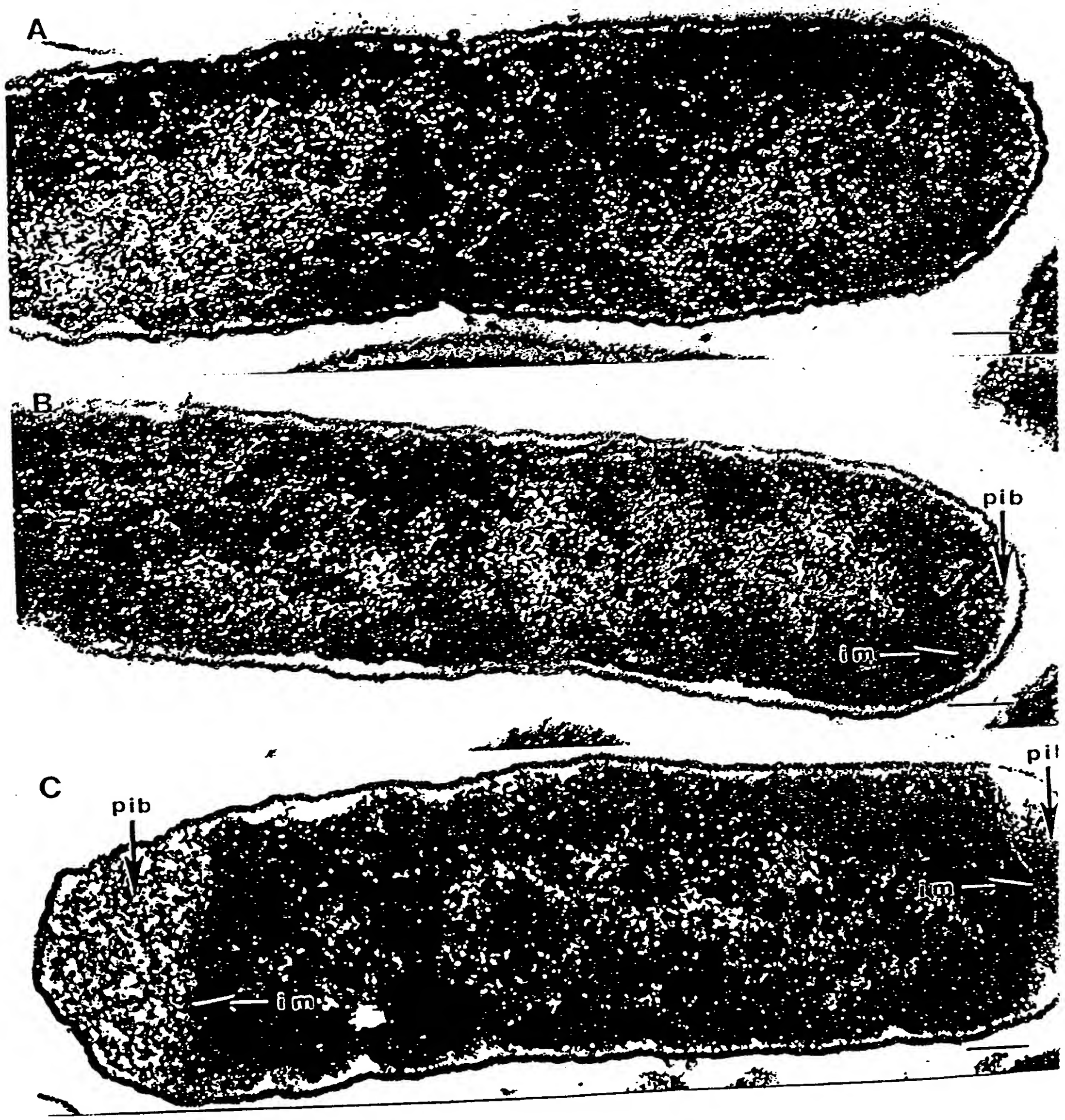


Fig. 7

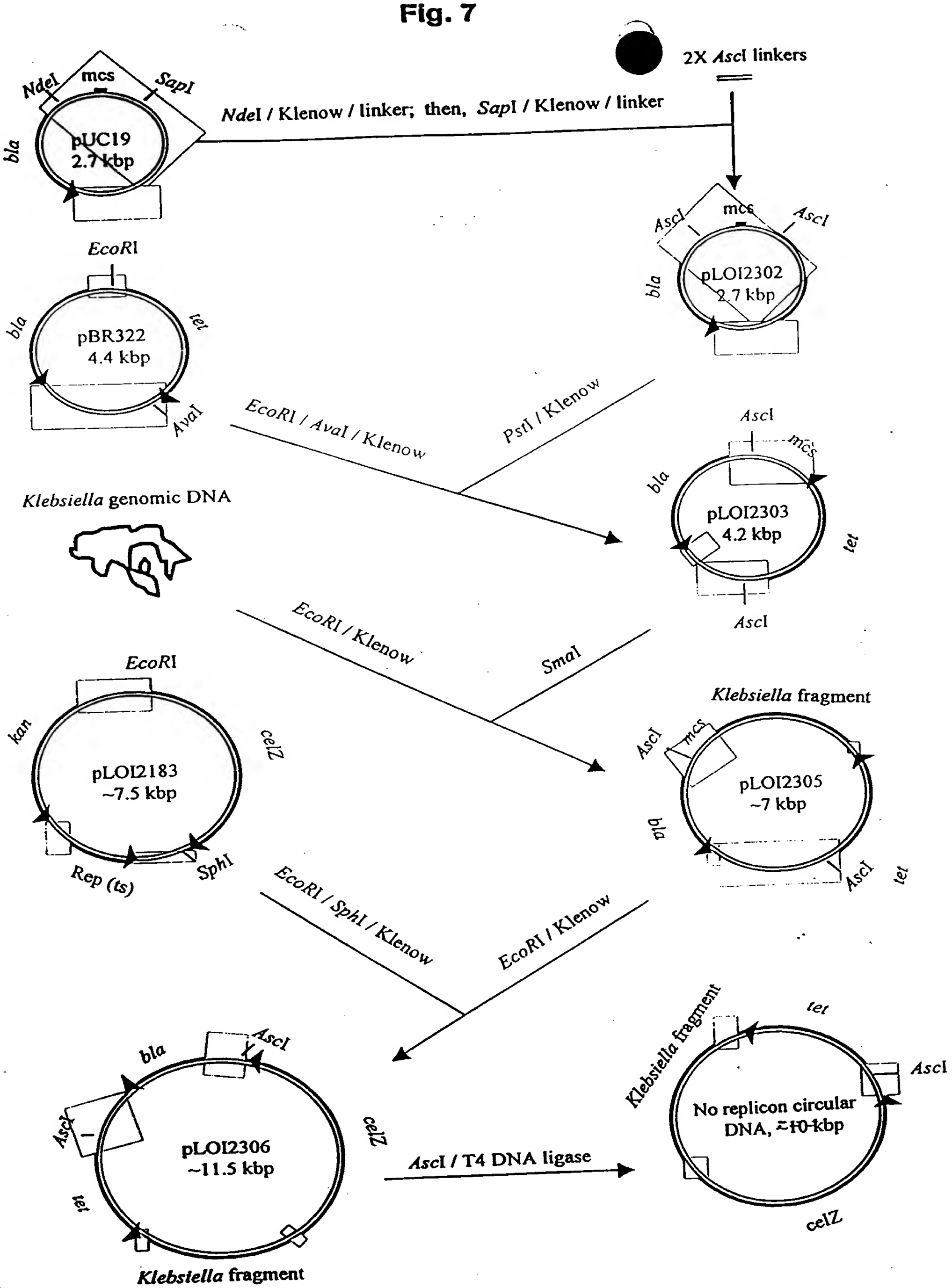
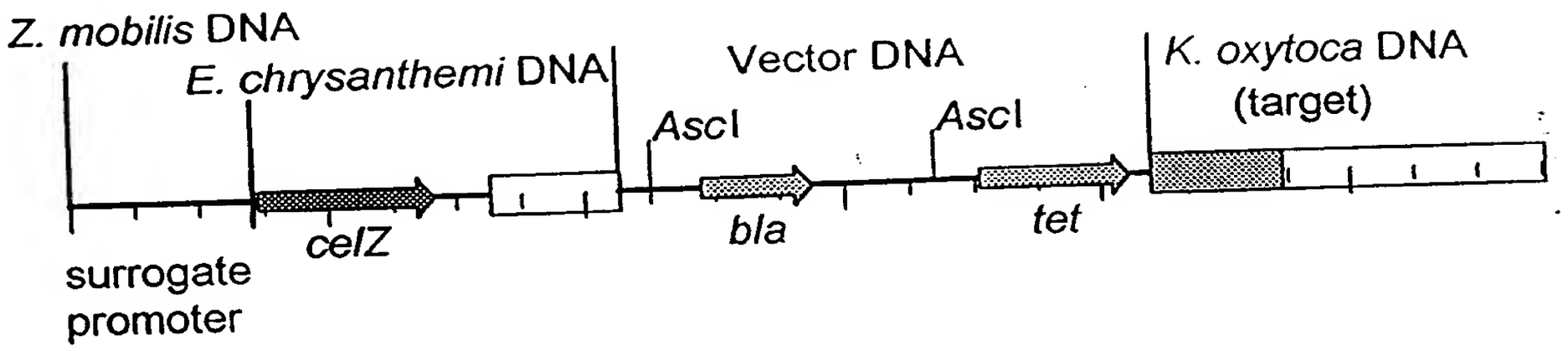
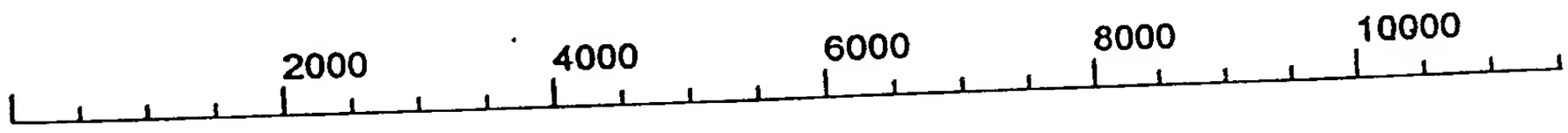

2X AscI linkers
NdeI
mcs
SapI
bla
pUC19
2.7 kbp
NdeI / Klenow / linker; then, SapI / Klenow / linker
AscI
mcs
AscI
bla
pLOI2302
2.7 kbp
EcoRI
bla
pBR322
4.4 kbp
tet
AvaI
EcoRI / AvaI / Klenow
PstI / Klenow
AscI
mcs
bla
pLOI2303
4.2 kbp
tet
AscI
Klebsiella genomic DNA
EcoRI / Klenow
SmaI
EcoRI
kan
pLOI2183
~7.5 kbp
celZ
Rep (ts)
SphI
Klebsiella fragment
AscI
mcs
pLOI2305
~7 kbp
bla
AscI
tet
EcoRI / SphI / Klenow
EcoRI / Klenow
bla
AscI
pLOI2306
~11.5 kbp
tet
celZ
Klebsiella fragment
tet
AscI
No replicon circular
DNA, ~10 kbp
celZ
AscI / T4 DNA ligase
Klebsiella fragment

Fig. 8





pLOI2306 (11520 bps)

Fig. 9

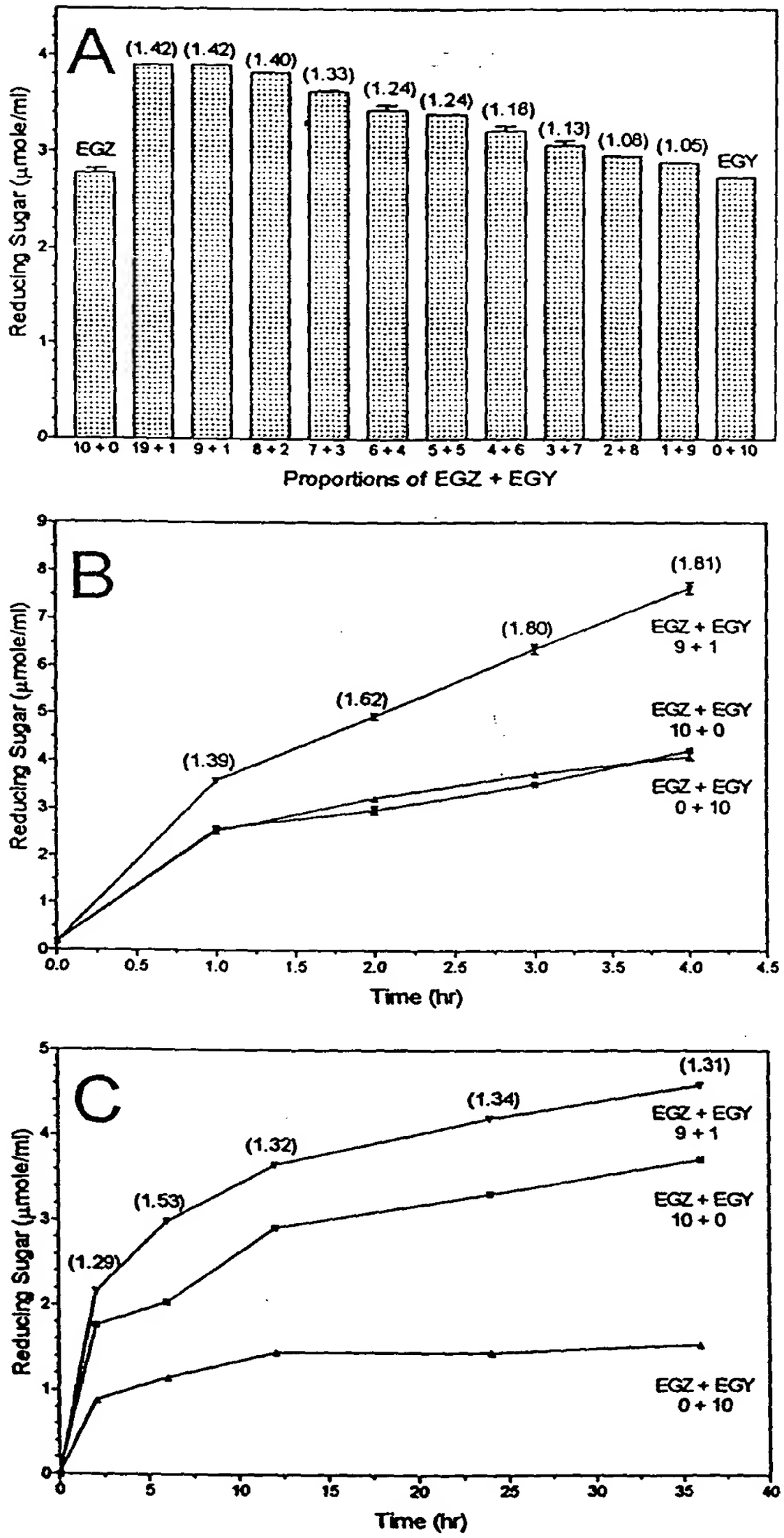

A
(1.42)
(1.42)
(1.40)
(1.33)
(1.24)
(1.24)
(1.16)
(1.13)
(1.08)
(1.05)
EGZ
EGY
Reducing Sugar (μmole/ml)
10 + 0
19 + 1
9 + 1
8 + 2
7 + 3
6 + 4
5 + 5
4 + 6
3 + 7
2 + 8
1 + 9
0 + 10
Proportions of EGZ + EGY
B
(1.81)
(1.80)
(1.62)
(1.39)
EGZ + EGY
9 + 1
EGZ + EGY
10 + 0
EGZ + EGY
0 + 10
Reducing Sugar (μmole/ml)
Time (hr)
C
(1.31)
(1.34)
(1.32)
(1.53)
(1.29)
EGZ + EGY
9 + 1
EGZ + EGY
10 + 0
EGZ + EGY
0 + 10
Reducing Sugar (μmole/ml)
Time (hr)

Fig. 10

Fig. 11

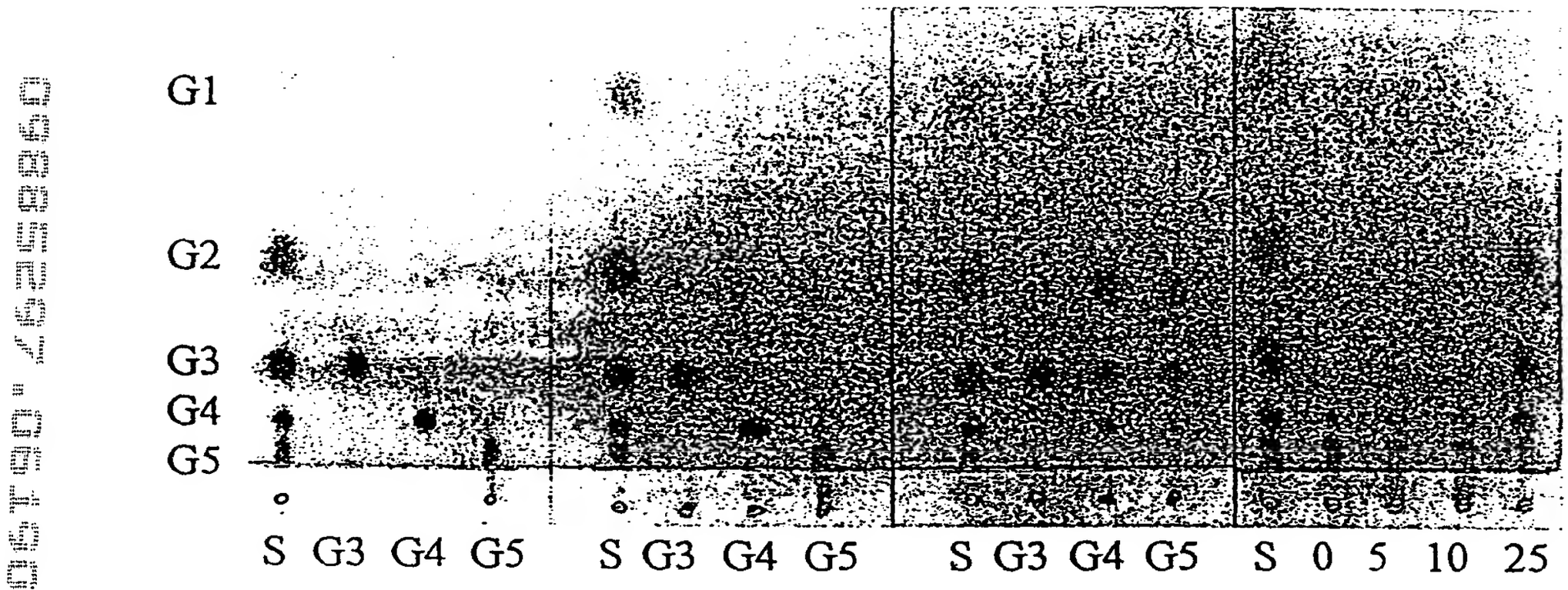


Fig. 12

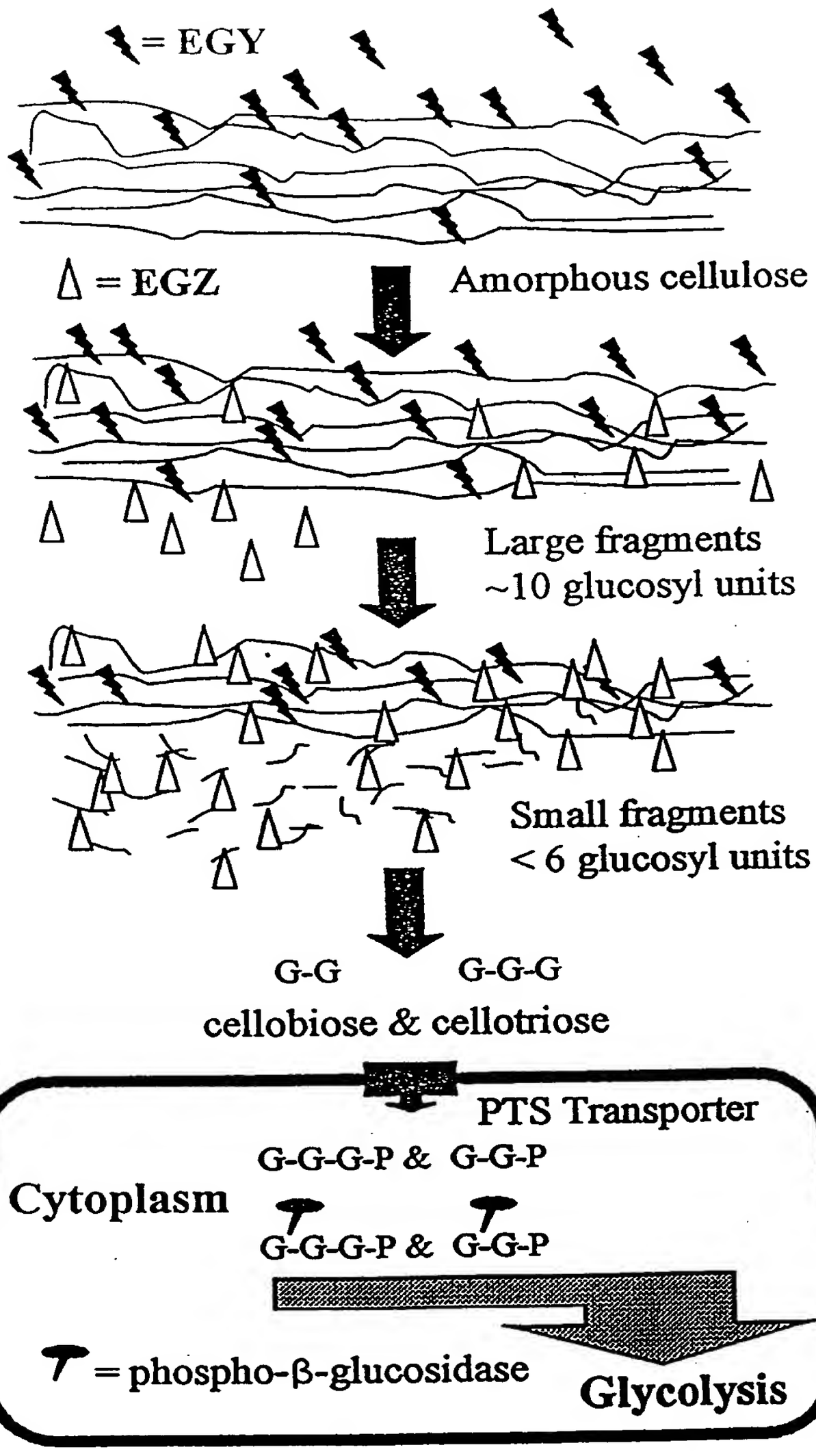
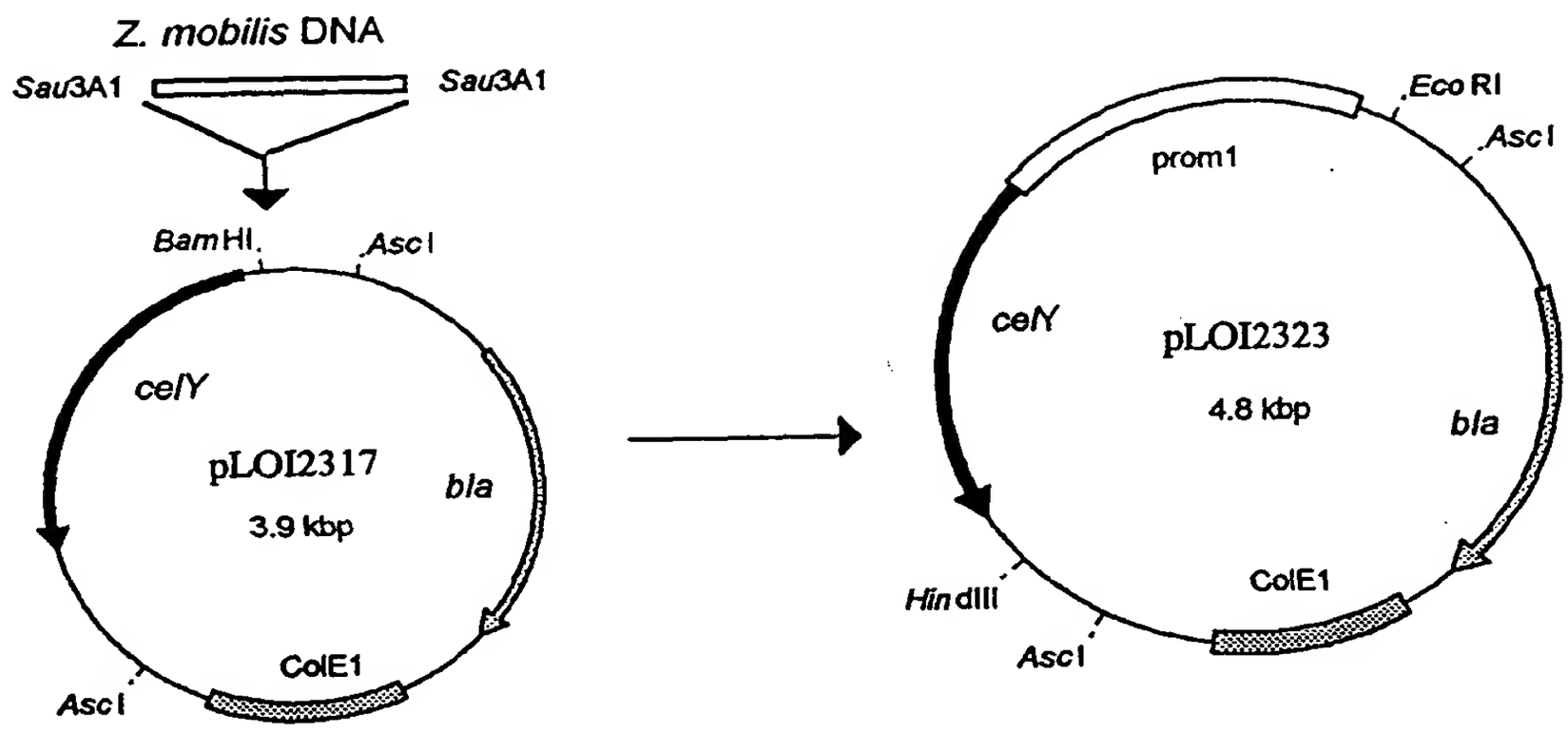

= EGY
= EGZ
Amorphous cellulose
Large fragments
~10 glucosyl units
Small fragments
< 6 glucosyl units
G-G
G-G-G
cellobiose & cellotriose
PTS Transporter
G-G-G-P & G-G-P
Cytoplasm
G-G-G-P & G-G-P
= phospho-β-glucosidase
Glycolysis

Fig. 13


Z. mobilis DNA
Sau3A1
Sau3A1
BamHI
AscI
celY
pLOI2317
3.9 kbp
bla
ColE1
AscI
EcoRI
AscI
prom1
celY
pLOI2323
4.8 kbp
bla
ColE1
HindIII
AscI

Position (bp)	-35	-10	RNA Start	Proposed δ factors	δ factor consensus sequence	
					-35	-10
	ATATTTTTGATTTTTCAAGAAAAGCCTGATATCTTCCAACATCTT		**T** (2)	δ^{70}	TTGACA	TATAAT
	GATTTGATCCTCTAGAGTCAACCTGCTTGTTACTCGTGATCCCAT		**A** (4)	δ^{70}	TTGACA	TATAAT
	GAGTCAACCTGCTTGTTACTCGTGATCCCATTCACAAGGGCGAA		**C** (1)	δ^{32}	CTTGAAA	CCCCAT
	TTACTCGTGATCCCATTCACAAGGGCGAATTAATTCGCCCTT		**C** (3)	δ^{38}	CCGCCT	TATACT

[a] Transcriptional starts for *celY* were identified by primer extension analysis. Four promoters were identified. Upstream sequence of these promoters with similarity to *E. coli* -35 and -10 regions are marked with underlines. RNA start sites are bolded. Putative promoters are numbered in parenthesis adjacent to the start site in decending order from the strongest. Differences in intensities were small, within 2-fold.

Fig. 14

Fig. 15

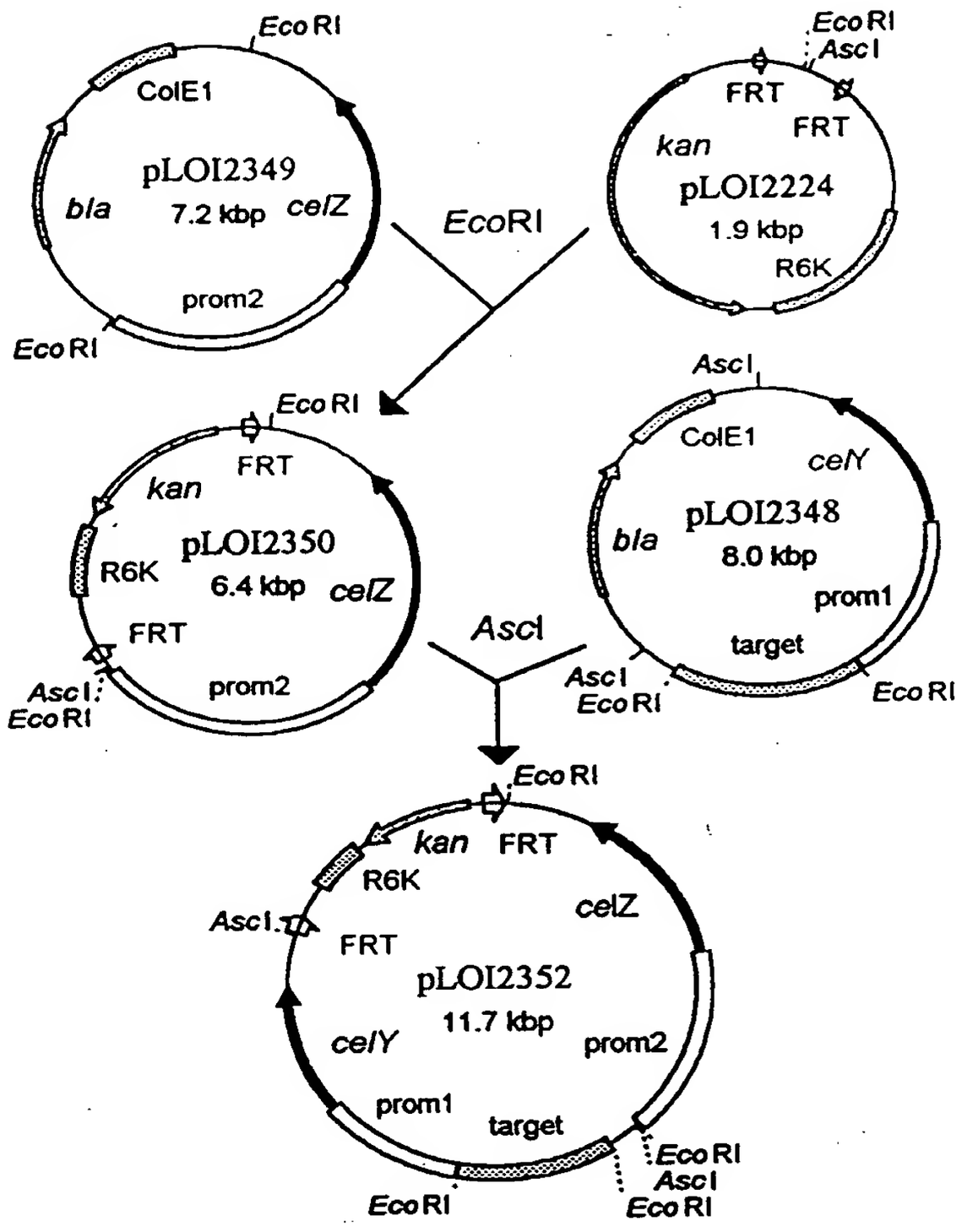

EcoRI
ColE1
pLOI2349
bla
7.2 kbp
celZ
prom2
EcoRI
EcoRI
AscI
FRT
FRT
kan
pLOI2224
1.9 kbp
R6K
EcoRI
AscI
ColE1
celY
pLOI2348
bla
8.0 kbp
prom1
target
AscI
EcoRI
EcoRI
EcoRI
FRT
kan
pLOI2350
R6K
6.4 kbp
celZ
FRT
prom2
AscI
EcoRI
AscI
EcoRI
EcoRI
kan
FRT
R6K
celZ
AscI
FRT
pLOI2352
11.7 kbp
celY
prom2
prom1
target
EcoRI
AscI
EcoRI
EcoRI

Fig. 16

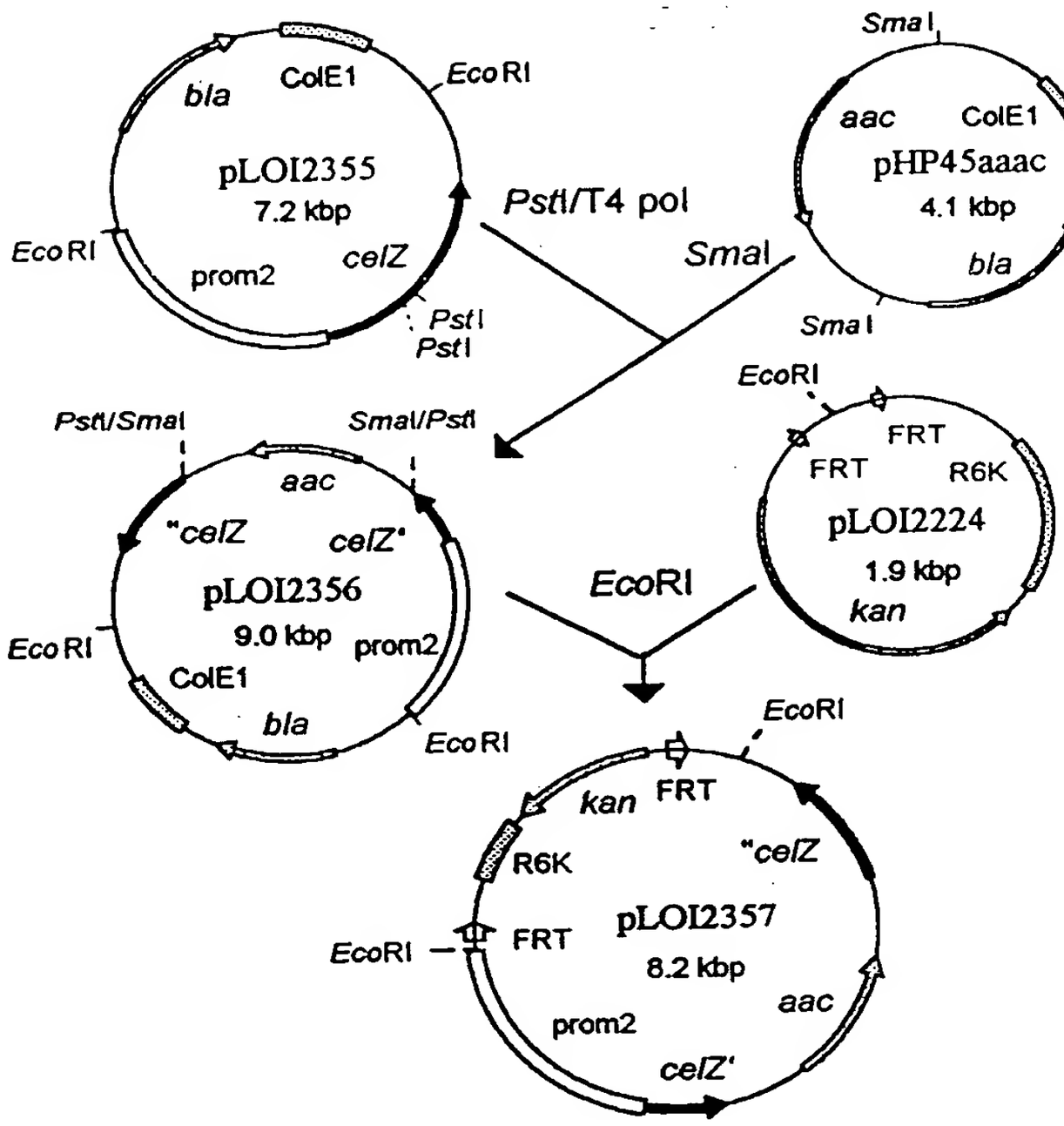

bla
ColE1
EcoRI
pLOI2355
7.2 kbp
EcoRI
celZ
prom2
PstI
PstI
PstI/T4 pol
SmaI
SmaI
aac
ColE1
pHP45aaac
4.1 kbp
bla
SmaI
PstI/SmaI
SmaI/PstI
aac
"celZ
celZ'
pLOI2356
9.0 kbp
prom2
EcoRI
ColE1
bla
EcoRI
EcoRI
FRT
FRT
R6K
pLOI2224
1.9 kbp
kan
EcoRI
EcoRI
kan
FRT
R6K
"celZ
pLOI2357
8.2 kbp
EcoRI
FRT
aac
prom2
celZ'

Fig. 17

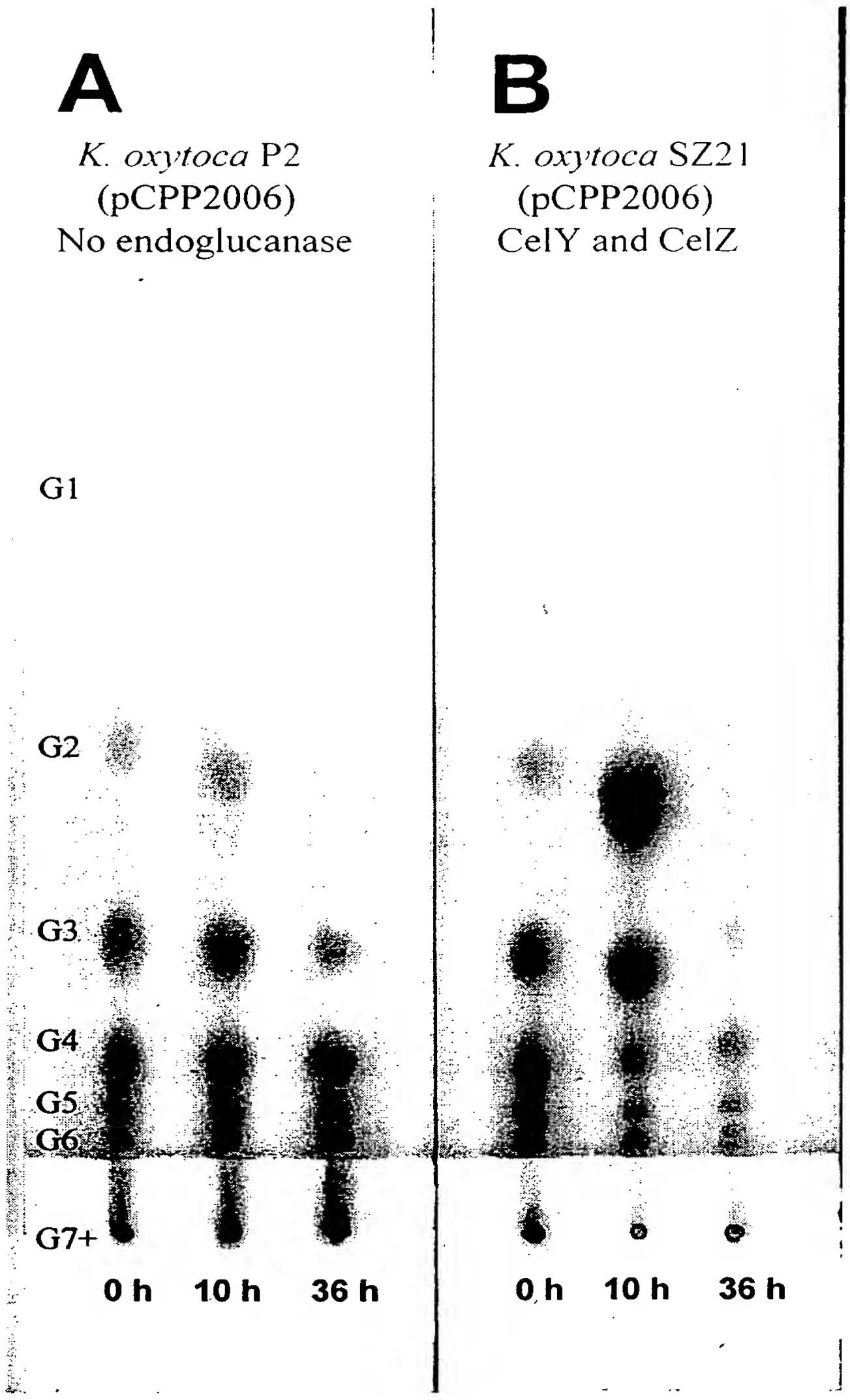
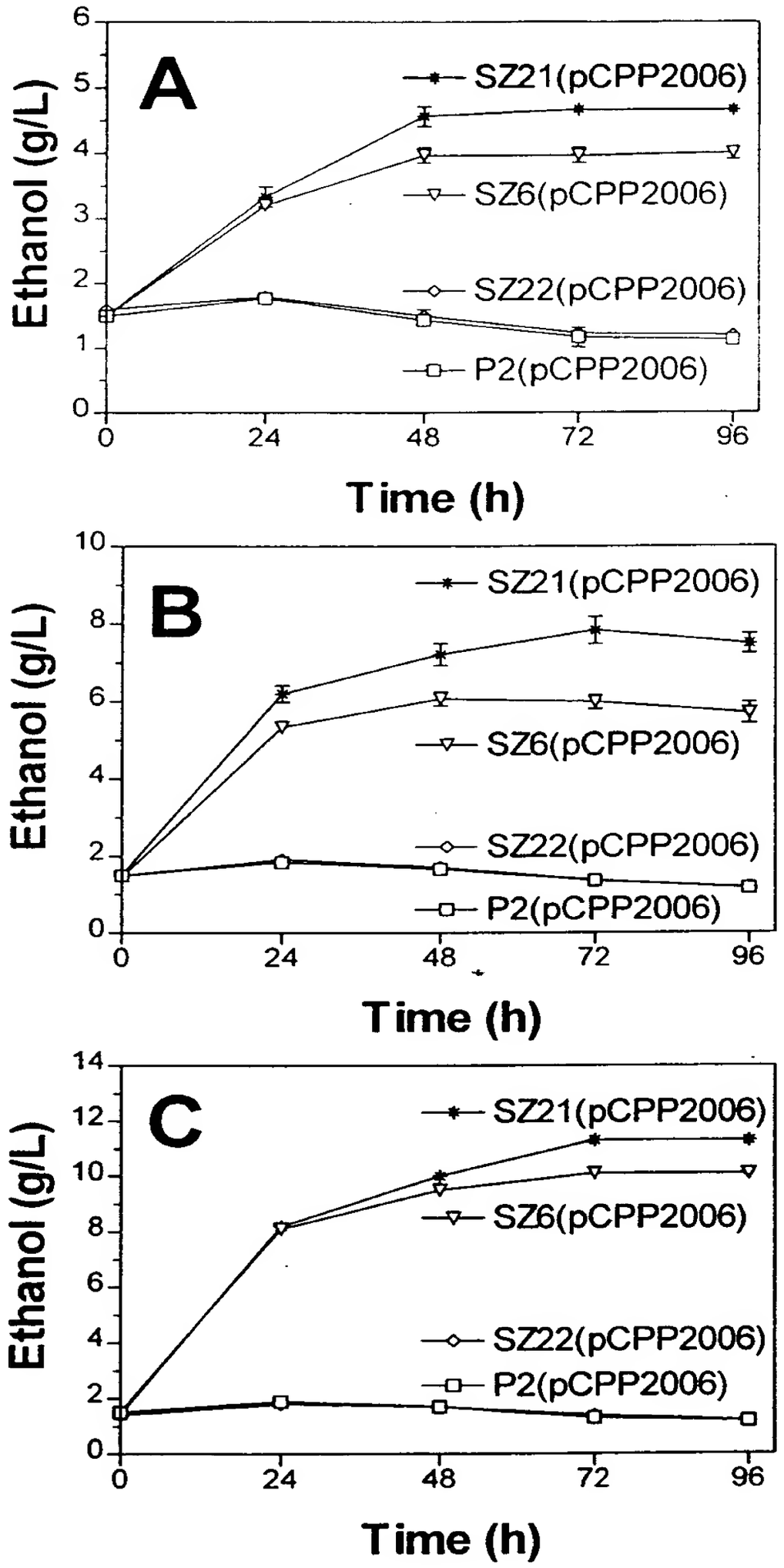

A
K. oxytoca P2
(pCPP2006)
No endoglucanase
B
K. oxytoca SZ21
(pCPP2006)
CelY and CelZ
G1
G2
G3
G4
G5
G6
G7+
0 h
10 h
36 h
0 h
10 h
36 h

Fig. 18


A
Ethanol (g/L)
Time (h)
SZ21(pCPP2006)
SZ6(pCPP2006)
SZ22(pCPP2006)
P2(pCPP2006)
0
1
2
3
4
5
6
0
24
48
72
96
B
Ethanol (g/L)
Time (h)
SZ21(pCPP2006)
SZ6(pCPP2006)
SZ22(pCPP2006)
P2(pCPP2006)
0
2
4
6
8
10
0
24
48
72
96
C
Ethanol (g/L)
Time (h)
SZ21(pCPP2006)
SZ6(pCPP2006)
SZ22(pCPP2006)
P2(pCPP2006)
0
2
4
6
8
10
12
14
0
24
48
72
96